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22. The method according to claims 20 or 21 wherein the fusion polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 10 and 12.
23. The method according to any one of claims 11 to 22 when used to enhance the phosphorus nutrition of a plant or the growth of a plant on a phosphorus source comprising phytate and/or increase the phosphorus content of a plant.
24. The method according to any one of claims 11 to 22 when used to enhance the biomass produced by a plant .
25. The method according to any one of claims 11 to 22 when used to enhance the rate of hypocotyl production or the rate of epicotyl production.
26. A transformed plant that ectopically expresses a secretable phytase polypeptide in its roots wherein said phytase polypeptide is secreted from the roots of said plant, wherein said plant is produced by a process comprising performing the method according to any one of claims 1 to 25.
27. Progeny of the transformed plant of claim 26 wherein said progeny ectopically expresses a secretable phytase polypeptide in its roots wherein said phytase polypeptide is secreted from the roots of said plant.
28. The transformed plant of claim 26 wherein said plant grows on a phosphorus source comprising phytate more efficiently than an isogenic plant that does not ectopically express the phytase enzyme.
29. The progeny of claim 27 wherein said progeny grows on a phosphorus source comprising phytate more efficiently than an isogenic plant that does not ectopically express the phytase enzyme.

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37. The process according to any one of claims 34 to 36 wherein the secretion of phytase from the root is achieved by ectopically expressing the phytase as a fusion protein with a secretory signal peptide.
38. The process according to claim 37 wherein the secretory signal peptide is selected from the group consisting of the carrot extension signal peptide and the lupin acid phosphatase signal peptide.
39. The process according to any one of claims 34 to 38 wherein the phytase polypeptide is from *Aspergillus niger*.
40. The process according to any one of claims 34 to 39 wherein the phytase polypeptide has at least about 93% identity to SEQ ID NO: 2.
41. The process according to claim 40 wherein the phytase polypeptide is selected from the group consisting of SEQ ID Nos: 2 and 4.
42. The process according to claim 40 wherein the phytase polypeptide is encoded by a nucleotide sequence selected from the group consisting of SEQ ID Nos: 1, 3 and degenerate nucleotide sequences thereto.
43. The process according to claim 5 wherein the phytase polypeptide is encoded by a nucleotide sequence contained within the plasmid assigned AGAL Accession No. NM99/06795.
44. An isolated nucleic acid molecule encoding a mature phytase polypeptide without a phytase leader sequence and comprising a nucleotide sequence selected from the group consisting of: (i) the nucleotide sequence of SEQ ID NO: 1 or 9; (ii) a nucleotide sequence encoding the amino acid sequence of SEQ ID NO: 2 or 10; and (iii) a sequence that hybridises to a phytase-encoding nucleotide sequence contained within the plasmid assigned AGAL

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Accession No. NM99/06795 or a complementary nucleotide sequence thereto under high stringency hybridisation conditions.

45. The isolated nucleic acid molecule of claim 44 comprising the nucleotide sequence set forth in SEQ ID NO: 1 or 9.
46. A gene construct comprising the isolated nucleic acid molecule according to any one of claims 44 or 45 placed operably in connection with a promoter sequence that is operable in the root cells of a plant.
47. The gene construct of claim 46 comprising the *PhyA-2* chimeric gene sequence set forth in SEQ ID NO: 1.
48. The gene construct of claim 46 comprising the *ext::PhyA-2* sequence set forth in SEQ ID NO: 9.
49. The gene construct according to claim 46 consisting of the plasmid assigned AGAL Accession No. NM99/06795 .

**AMENDED CLAIMS**

[received by the International Bureau on 19 January 2001 (19.01.01);  
original claims 26, 44-49 amended; remaining claims unchanged (3 pages)]

22. The method according to claims 20 or 21 wherein the fusion polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 10 and 12.
23. The method according to any one of claims 11 to 22 when used to enhance the phosphorus nutrition of a plant or the growth of a plant on a phosphorus source comprising phytate and/or increase the phosphorus content of a plant.
24. The method according to any one of claims 11 to 22 when used to enhance the biomass produced by a plant .
25. The method according to any one of claims 11 to 22 when used to enhance the rate of hypocotyl production or the rate of epicotyl production.
26. A transformed plant that ectopically expresses a secretable phytase polypeptide in its roots wherein said phytase polypeptide is secreted from the roots of said plant, wherein said plant is produced by a process comprising performing the method according to any one of claims 1 to 25.
27. Progeny of the transformed plant of claim 26 wherein said progeny ectopically expresses a secretable phytase polypeptide in its roots wherein said phytase polypeptide is secreted from the roots of said plant.
28. The transformed plant of claim 26 wherein said plant grows on a phosphorus source comprising phytate more efficiently than an isogenic plant that does not ectopically express the phytase enzyme.
29. The progeny of claim 27 wherein said progeny grows on a phosphorus source comprising phytate more efficiently than an isogenic plant that does not ectopically express the phytase enzyme.

37. The process according to any one of claims 34 to 36 wherein the secretion of phytase from the root is achieved by ectopically expressing the phytase as a fusion protein with a secretory signal peptide.
38. The process according to claim 37 wherein the secretory signal peptide is selected from the group consisting of the carrot extension signal peptide and the lupin acid phosphatase signal peptide.
39. The process according to any one of claims 34 to 38 wherein the phytase polypeptide is from *Aspergillus niger*.
40. The process according to any one of claims 34 to 39 wherein the phytase polypeptide has at least about 93% identity to SEQ ID NO: 2.
41. The process according to claim 40 wherein the phytase polypeptide is selected from the group consisting of SEQ ID Nos: 2 and 4.
42. The process according to claim 40 wherein the phytase polypeptide is encoded by a nucleotide sequence selected from the group consisting of SEQ ID Nos: 1, 3 and degenerate nucleotide sequences thereto.
43. The process according to claim 5 wherein the phytase polypeptide is encoded by a nucleotide sequence contained within the plasmid assigned AGAL Accession No. NM99/06795.
44. An isolated nucleic acid molecule encoding a mature phytase polypeptide without a phytase leader sequence and comprising a nucleotide sequence selected from the group consisting of: (i) the nucleotide sequence of SEQ ID NO: 1 or 9; (ii) a nucleotide sequence encoding the amino acid sequence of SEQ ID NO: 2 or 10; and (iii) a sequence that hybridises to a phytase-encoding nucleotide sequence contained within the plasmid assigned AGAL

Accession No. NM99/06795 or a complementary nucleotide sequence thereto under high stringency hybridisation conditions.

45. The isolated nucleic acid molecule of claim 44 comprising the nucleotide sequence set forth in SEQ ID NO: 1 or 9.
46. A gene construct comprising the isolated nucleic acid molecule according to any one of claims 44 or 45 placed operably in connection with a promoter sequence that is operable in the root cells of a plant.
47. The gene construct of claim 46 comprising the *PhyA-2* chimeric gene sequence set forth in SEQ ID NO: 1.
48. The gene construct of claim 46 comprising the *ext::PhyA-2* sequence set forth in SEQ ID NO: 9.
49. The gene construct according to claim 46 consisting of the plasmid assigned AGAL Accession No. NM99/06795 .